

104680

GenCore version 5.1.3
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On nucleic - nucleic search, using sw model
Run on: November 30, 2002, 07:42:58 ; Search time 384 Seconds

(without alignments) 16221.425 Million cell updates/sec

Perfect score: 2766

Sequence: 1 atgcgcgtgttaaagggttgc.....gtacatcaagggttctaa 2766

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database 8 NGenesca1010028*

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RESULT 1
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ID ABN83428 standard; cDNA; 2782 BP.
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AC ABN83428;
XX
DT 21-AUG-2002 (first entry)
XX
DE Human transporter protein coding sequence.
XX
KW Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;
spleen; testis; leukocyte; foetal brain; chromosome 14; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200233086-A2.

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	2761.2	99.9	2762	24 ABN83429 Human transporter Human transporter (H)-C
2	2761.2	98.3	27681	24 ABA04756 Human transporter Human heart cells Human ORF1261
3	1784.8	64.5	12512	24 ABN83429 Human transporter Human heart cells Human NCX-1 cDNA
4	1326.4	48.0	2814	22 AAH5777 Human transporter Human heart cells Human ORF1261
5	1277.8	46.2	4291	21 AAC7506 Human transporter Human heart cells Human NCX-1 cDNA
6	1227.8	44.4	4087	24 AAD2450 Human transporter Human heart cells Human NCX-1 cDNA
7	1208.8	43.7	4338	23 ABV24305 Human transporter Human heart cells Human NCX-1 cDNA
8	897.4	32.4	1187	23 AAS90568 Human transporter Human heart cells Human NCX-1 cDNA
9	787.2	28.5	1836	22 ABA64480 Human foetal liver

Pred. No. 1 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2761.2	99.9	2762	24 ABN83429 Human transporter Human transporter (H)-C
2	2761.2	98.3	27681	24 ABA04756 Human transporter Human heart cells Human ORF1261
3	1784.8	64.5	12512	24 ABN83429 Human transporter Human heart cells Human NCX-1 cDNA
4	1326.4	48.0	2814	22 AAH5777 Human transporter Human heart cells Human ORF1261
5	1277.8	46.2	4291	21 AAC7506 Human transporter Human heart cells Human NCX-1 cDNA
6	1227.8	44.4	4087	24 AAD2450 Human transporter Human heart cells Human NCX-1 cDNA
7	1208.8	43.7	4338	23 ABV24305 Human transporter Human heart cells Human NCX-1 cDNA
8	897.4	32.4	1187	23 AAS90568 Human transporter Human heart cells Human NCX-1 cDNA
9	787.2	28.5	1836	22 ABA64480 Human foetal liver

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Probe #10085 for g

Human brain expres

Probe #9397 for ge

Probe #1343 used

Human genome-deriv

Drosophila melanog

Human polyrnucleoti

Drosophila melanog

Human breast cell

Human foetal liver

Probe #1172 for ge

Human brain expres

Human bone marrow

Probe #1197 for ge

Probe #616 for ge

Human breast cell

Human brain expres

Human bone marrow

Probe #658 for gen

Probe #679 used to

Probe #654 used to

Human genome-deriv

Human brain expres

Human bone marrow

Human brain expres

Human bone marrow

Human brain expres

PI	Besley EM;	Db	730	TTTCAGGTGGCTCTTCGGCTGGGGAGATAACAGACTGCCTCTCACAAATAC	789
XX		Qy	781	ATGCACAAAAAGTACCSACAGACAAACCCAGGAATTATAGAGACAGGGTGAC	840
DR	WPI: 2002-479677-31.				
DR	P-PSDB; ABB83246.	Db	790	ATGCACAAAGTACCGACAGACAAACCCAGGAATTATAGAGACAGGGTGAC	849
XX	Human transporter peptide related to sodium/calcium exchanger subfamily				
PT	for identifying modulators useful for treating a disease or condition				
PT	mediated by human transporter protein				
XX	Claim 4; Fig 1; 20pp; English.				
PS					
XX					
CC	The present sequence is the coding sequence of a human transporter				
CC	protein, which is related to the sodium/calcium exchanger subfamily.				
CC	Experimental data indicates expression of the transporter gene in humans				
CC	in brain, heart, kidney, lung, spleen, testis, leukocyte and foetal				
CC	brain. The gene of the transporter was mapped to chromosome 14 by ePCR.				
SQ	Sequence 2782 BP: 655 A; 685 C; 766 G; 676 T; 0 other:				
	Query Match 99.8%; Score 2761.2; DB 24; Length 2782;				
	Best Local Similarity 99.9%; Pred. No. 0;				
	Matches 2763; Conservative 0; Mismatches 3; Indels 0; Gaps 0;				
Qy	1 ATGGCGTGTAAAGGTTCAGGCTCTCACCTGCTCTCCATTGGGCGGTAC	Qy	841	CACCTTAAGGGCATGGATGGATGGAAATGATGATTCATTTCTAGATGGAAAC	900
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Qy	61 TTTGTGCHCTCTCTGAAAGTGTCTCGACCTCGCCCTCTCAATTGGGGTAC	Qy	901	CCTGGCCCTGGAGGAGGAGGTGGATGACTCCGGAGAGATGATCCGGATCTC	960
Db	70 TTGTGCHCTCTCTGAAAGTGTCTCGACCTCGCCCTCTCAATTGGGGTAC	Db	910	CTTGTGCCCTGGAGGAGGAGGTGGATGACTCCGGAGAGATGATCCGGATCTC	969
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Qy	181 CCACATCGTACCCGGAGAACCTTCCCTGGGACAGAAGATGCCAGGTCATGCTAT	Qy	1021	TACTATGCTTTCACCAAGAAGAGAGGCGCCCTCTACGGTATCCAAAGCCACTCTG	1080
Db	190 CCACATCGTACCCGGAGAACCTTCCCTGGGACAGAAGATGCCAGGTCATGCTAT	Db	1030	TACTATGCTTTCACCAAGAAGAGAGGCGCCCTCTACGGTATCCAAAGCCACTCTG	1089
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Db	250 TTGTGCGCTGTATACTATGTTCTGGGTATCCATGCTGTGACCGCTCATGGCA	Db	1090	ATGATGACTGGTCCAGGCAATCTCTGAAAGAACATCGCAGAACAGCCAGAAGGCC	1149
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Db	370 ACCAGCNAACCCATATGGGGCTGGATGAAACTGTCTCCACCTGACCCCTATGCC	Db	1210	GACCCATGTCCTACCGAGTGCCTGAGAACCTGAGGAGGAGCTGAGCTGAGTGGAGG	1269
Qy	421 CTGGGTCT	Qy	1261	AAAGGGAGACATGTCAGAACACCATGTTGAGGACTACAAACAGAGGATGGTCTGC	1320
Db	430 CTGGGTCT	Db	1270	AAAGGGAGACATGTCAGAACACCATGTTGAGGACTACAAACAGAGGAGCTGCG	1329
Qy	481 ATGGCTGTGATCTGGACCTTCTACCATGTTGGAGTCAGCTTCACATGTCATC	Qy	1321	ATGCGAGGGCTGACTATGAGTCACAGAGGGCACGGTGTCTGAAGCAGGAGAC	1380
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Db	670 CTGGCAGTCCT	Db	1510	GCATATTCACAGTCGCTCCCTGCCGCGGCTGCTCTAGCCCTCTGGCCACA	1569
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Db 2623 TACCGAGGGGGCCACCTGGAGGGGCTGGGCCCTGGCTGGCTGGCTGGCTGGCTGG 2682
Db 2641 TACCGAGGGGGCCACCTGGAGGGGCTGGGCCCTGGCTGGCTGGCTGGCTGGCTGG 2700
Db 2683 ACAACTGGCTTGTGAGCTGTGCTCTACATACACTCTTGCACTAGAGGCC 2742
Db 2701 ACAACATGGCTTGTGAGCTGTGCTCTACATACACTCTTGCACTAGAGGCC 2760
Db 2743 TATTGCTACATCAAGGGTTC 2763
Db 2761 TATTGCTACATCAAGGGTTC 2781

RESULT 3
ABN83429 standard; DNA; 126512 BP.
AC ABN83429;
XX DT 21-AUG-2002 (first entry)
XX DE Human transporter protein gene.
XX KW Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung; spleen; testis; leukocyte; foetal brain; chromosome 14; gene; single nucleotide polymorphism; SNP; os.
XX OS Homo sapiens.

Key
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Qy	589	ATCAGCATCTAGAGTCCTCTCATCACCGCTCTGGAGATCTTGCCATACATCGG	648
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Db	1492	GTCAAGATCTCTGAGACCTTCAGAGATGGCATACTGGAAG	1542
Qy	1519	CCCTGGCTCTGGCTCTAGCTCCCTGTTGGGCCACAGTACCATCTGGATCA	1578
Db	1543	GTTCCTACACTGCTGCCCTGGATCCTCCACTGCCCCACTGACTAATTTTGATGAT	1602
Qy	1579	GACCATGCGGCACTCTGCACTTTGAGATGAGTACTATCATGAGAGTATGG	1638
Db	1603	GACCAAGGGCATTTTACTTTGAGGACCTGTGACTCATGAGGAGCATGG	1662
Qy	1639	GTATGGGGCTCAAGGTTGGGACATCAGGCGCCGGGTACACTCATGCGCCCTT	1698
Db	1663	ATCATGAGGTGAAGATTTGAGACATCTGGAGCTCGAGAAATGTTATGTTCCAT	1722
Qy	1699	AGGAGTGAAGGACACCAAGGGGGGGTGGAGGACTTGAAGACACATATGGGAG	1758
Db	1723	AAACCATGAGGACGCCAGGGGGGGTGGAGGACTTGAAGGAGCTGAGCTG	1782
Qy	1759	TGGAATTCAGAATGATGAACTGAAACCATAGGTTAAATAGTAGATGAGGAG	1818
Db	1783	CTCGAACTCAGAATGATGAAATGAGATCATACCATTTGAGATTTGACCGTGAG	1842
Qy	1819	GAATACGAAAGGAGAGAATTTCTCATGCGCTTGTGAGGAAATGGTGAACGT	1878
Db	1843	GAATATGAGAAAGAGTGCCTCTCCCTGTCGTTGAGAACAAATGGATAAGAGA	1902
Qy	1879	GGATATCG-----	1914
Db	1903	GGATGAAGGCTCACAATTACAGACAAATTGATGACAGACAAATGATGACAG	1962
Qy	1915	GAAGAGAGGGGCAAGAGGATGAGGATGAGGAAAGCCACTATGGTGAACACCC	1974
Db	1963	AAAGAGGAAGGAGGCCATGAGAAATGGGGCCCTCTGGAGGAGGAGCAC	2022
Qy	1975	AAACTAGAGTCACTGAGGAGTCTGAGGCTCTGAGTACGGTGGAGAACACT	2034
Db	2023	AAGTGGAGAGTGCATCTGAGGATCTGAGGATCTGAGGAGAACATGACGAAACTCAT	2082
Qy	2035	AAGAGACAAACCTGGCTTGGCTGTCGAGGACATTCAGAGTACTGTGGAGA	2094
Db	2083	AAGAGACAAACCTGGCTTGGCTGTCGAGGACATTCAGAGTACTGGAGAAGACAG	2142
Qy	2095	GCATCACGGCTAGTCAGCAGCAGGGATGGGGATGAGGATGAATCAGGAGGAGGCTG	2154
Db	2143	GCTATCACTGTCAGTCGGGGAGATGAGACGAGGAGTAACTGGGGAGAGAAG	2202
Qy	2155	CCCTCTGTTGACTGACTGACTGACTGACTCTCTGAGTGGGAGGCTGCTG	2214
Db	2203	CCCTCTGTTGACTGACTGACTGACTCTCTGAGTGGGAGGCTGCTG	2262
Qy	2215	TGCTGCCCCACAGAATGACTGCTGACGCTGTCGCTGGCCCTCCGCTCCATC	2274
Db	2263	TTGCTCCCCCTACTGAAATTACTGAAATGCTGGGCTGTTCTGCTCCATC	2322
Qy	2275	ATTGGCATGCTCACGCCCATGGGACCTGGCTGGCTGGCTGGCTGACCTGGT	2334
Db	2323	ATTGGCATGACTGACAGCTTCATGGAGACCTGGCTTCCACATTGGGACCAT	2382
Qy	2335	CTCAAGATTCAGTCAGCAGCTGCTGGGCTGAGCTGCTGGCTGAGCCTCAT	2394
Db	2383	CTGAAAGATTCAGTCAGCAGCTGCTGGGCTGAGCTGCTGGCTGAGCACA	2442
Qy	2395	TTGCCACCAAAGCCTGCTGCCCTCAGATGAGTATGAGGAGCTGCTGAG	2454
Db	2443	TTGCCACCAAAGCCTGCTGCCCTCAGATGAGTATGAGGAGCTGCTGAG	2502
Qy	2455	ACGGCAGAACGCCGCTGAGCTGCTGGCTGAGCTGCTGAGCTGCTGAG	2514
Db	2503	ACGGCAGAACGCCGCTGAGCTGCTGGCTGAGCTGCTGAGCTGCTGAG	2562
Qy	2515	ATCTACTGGCTGAGGAGGAGCTGGCTGAGCTGCTGGCTGAGCTGCTGAG	2574
Db	2563	ATCAGGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG	2622
Qy	2575	GTACCCCTCACCATTTGCTGAGGAGCTGAGCTGAGCTGAGCTGAGCTGAG	2634
Db	2623	GTCACTCTTCCACCATTTGCTGAGGAGCTGAGCTGAGCTGAGCTGAG	2682

FT	CDS	268..3180	Db	667 CTGACCTTGATGCCCTGGGCTTCAGCTAGAGATTCCTTCAGTAATGGGTR
FT		/*tag= a	Db	667 CTGACCTTGATGCCCTGGGCTTCAGCTAGAGATTCCTTCAGTAATGGGTR 726
FT		/product= "Bovine NCX-1 protein"	Db	466 TGTGGTCATGGTCATTGCGTGTGTCCTGGACCTTCATCATGTAGGGAGTCAGCC 525
XX			Db	727 TGTGGCTTACATTCACCTGAGGAGGCTTACCCATGGGGAGTCAGCC 786
PN	WO200206464-A2.		Db	526 TTCAGCATGTCATCATCATATGGCATCTGTTGCTAGGATTCAGCTTCAGCC 585
PD	24-JAN-2002.		Db	787 TTCAACATGTCATCATCATATGGCATCTGCTGGGAGTCAGCC 846
XX			Db	586 AAGATCAGCTTACAGACTTCATACCCATGGGGAGTCAGCC 645
PT	09-JUL-2001; 2001WO-US21606.		Db	847 AAGATCAGCTTACAGACTTCATACCCATGGGGAGTCAGCC 906
XX			Db	646 TGGCTTATATGATCTGCGAGTCCTCTCCCTGGTGTGTCAGCAGCAGTC 705
DR	13-JUL-2000; 2000US-218125P.		Db	967 TGGCTTATACATTTTGTCTGCTACCTCCCTGGGGAGTCAGCC 966
PT	P-PSDB; AAC18291.		Db	907 TGGCTTATACATTTTGTCTGCTACCTCCCTGGGGAGTCAGCC 1026
XX			Qy	765 CTCTCTACAAATCATGCACAAAGTACGCCAGACAGAACCGGAAATTCTATA 825
PS	Example 1; Page 31-37; 40pp; English.		Db	1027 CTGTTTACAGTATGTCATCAAGAGGTATGGGCTGGCAGACGGGATGTT 1086
XX			Qy	826 GAGACAGGGTGCACCC-----TAAGGGATGATGGATGGTGGGAAATGATG 876
CC	The patient discloses methods of producing recombinant proteins in larvae expression system, by infecting the larvae with vector having a sequence encoding recombinant fusion protein with affinity tag. The methods are useful for producing recombinant protein, preferably membrane proteins, transport proteins such as NCX1 (cardiac sodium calcium exchange protein) or Na ⁺ K ⁺ ATPase, channel forming proteins such as cystic fibrosis transmembrane conductance regulator (CFTR), junctional protein (connexin 32), receptor, cytoskeletal and other membrane associated proteins. They are also useful for producing prostate specific membrane antigens and sodium phosphate co-transporters from kidney. The methods are also useful for producing recombinant fusion proteins in large quantities that are both highly homogenous and biologically active. The recombinant proteins produced by the methods of the invention can be included as part of a pharmaceutical, nutritional, drug or vaccine composition. The present sequence is a cDNA encoding bovine NCX-1 protein.		Db	1087 GAACAGAAGAGCAGGCCACTTCACAGACAGAATGAAATGGATGGATGGTC 1145
CC			Qy	877 AATTCCATTTC-----TAGATGGAACCTGGTGCCTCTGAAAGGAAAG 921
CC			Db	1147 AATCCCATGTTGACAGTTCTTAGATGGACCCCTGGTCTGGAGGGAC 1206
CC			Qy	922 --GAATGGTGTAGTGCSCCAGAGATACCCGATTCAGATGGAAAG 978
CC			Db	1207 CAAGATGATGAGAAGCCAGCGAGAAATGGATCTGAGGAC 1266
CC			Qy	979 CACCGAGGAGACTTAGATCAGCTGGAGATGCCAATACATGCTCTTCCCAC 1038
XX			Db	1267 CATCCAGAGGAATAGACAAATTAAGATGAACTTAACTGAC 1326
SQ	Sequence 4087 BP; 1057 A; 950 C; 1057 G; 1023 T; 0 other;		Qy	1039 CAACAGAGACGCCCTTCACGTTACGGTATCAGGCACCTGATGCTGGTCAGGC 1098
Query	Match 44.4%; Score 1227.8; DB 24; Length 4087;		Db	1327 CAGCAGAAAGTCGAGCGTTTACGGTATCAGCTACCCCTGATGACGGAGCAGC 1386
Best Local Similarity	67.1%; Pred. No. 0;		Qy	1099 AATATCCTGAGAAACATGAGCAGAACAGCAAGAAGGCTCCAGCTGAGGAGTC 1158
Matches	1935; Conservative 0; Mismatches 777; Indels 171; Gaps 7;		Db	1387 AACATTTAAAGAGGCATGAGCAGACCAAGCAGCAGTCAGTCAGTCAGTCAGTC 1446
Qy	46 TTGGCTCTGGTACCTTGGCTCTTCGTGATGGTCATGGTACCCAGAACCTTCCTGGGACAGATGCC 105		Qy	1159 CACACGGATGACCTG---AGACCTTTACCAAGGTCTCTTGACCCATGTC 1215
Db	307 TTTCAGCTGATGAGCCATGGCTCTGGCTCTGGTACCCATATAGTGCTGAG 366		Db	1447 AACACGGAACTGGCAGAAATGACCCCTGAGTAAATGGAAAGGACAT 1506
Qy	106 GGGAGCTGCCAACACAGGGAGAACAACTGTCCTGTCAGGGTCATGGACTGCAAG 165		Db	1507 CAGTGTGGAGACTGGCACAGTACCCCTGACCATATCCGGAGGGGAGTTG 1566
Db	367 ACAGAAATGGAGGAGAACCAACGAGACTGGAGTGACTGGTCTCTTACGTAG 426		Qy	1216 CAGTGTGGAGACTGGGGCTGTACTCTGACAGTGTGGAGAACGGGAGACAT 1275
Qy	166 GAGGGTGTCACTCTGCCAACCTGTTGGTACCCAGAACCTTCCTGGGACAGATGCC 225		Db	1567 ACCACACTGTTGTTGACTTCAGACAGAGGAGGACGCCATGTCAGTC 1626
Db	427 AAGGGGTGATTTACCCATTGGGAGGCCCTCCCTGGAGAACAAATTGTG 486		Qy	1336 TATGAGTTCAGAGGGAGGTGTGAGCTGAGGAGGAGACCCAGGAGGAGTC 1395
Qy	226 AGGGCATTTGCTTATTTGGGCCCTGATATACAGTGTCTGGGTGTCATCATGGT 285		Db	1627 TACGATTTACCGAGGAGACTGGCTCTTAAGCTGGTGAAGCCAGGAATCA 1686
Db	487 AGAGCAGCTGTTGTTGTCAGCTACATCTGTCATCATGTCATCATGTC 546		Qy	1396 GTGGGATATTGATGACGACATTGAGGAGGAGACACTCTTGTAGGTGAGC 1455
Qy	286 GACCGCTTCATGGCATCTATGGAGTCATCACTCTCAAGAGGGGGCAATTAAG 345		Db	1687 GTGGCATCTGATGATGACATCTGAGGAGGATTCCTGTCATCTCAGC 1716
Db	547 GACCGCTTCATGGCATCTATGGAGTCATCACTCTCAAGAGGGGGCAATTAAG 606		Qy	1456 AATGTCGGCATAGAGGAGGAGCAGGGAGGAGGATGCTCCAGCAATTAACAGT 1515
Qy	346 ARACCAATGGAAACCGACCAACCACTATTCGGCTCGGAGAACCTGTCAC 405			
Db	607 AACCCCATGGAGACCCACCAAGACACTGTGGAGATGAGACAGAGTCAC 666			
Qy	406 CTGACCTTATGGCCCTGGGTTCTGCTCCTGAGAGATACTCCTCTTAA 465			

Db	1747	AACGTCAAAGTACCTTGGAAAGGCTCGAAAGGGCACCTCGAAAGC-----CAGT	1797	QY	2464	AAGCCCGGAAATGCTCTGGGCACTCGGCCCTGGCGCTGGGCCACATCTGG	2523
Qy	1516	CTTCCTCTGGCTGGCTGCTTACGCCCTGGCTGCTTACCTCTGGAT	1575	Db	2878	AACGGGGTAACTCTCTGGGATCGGGCTCGGCTCGGCCATCGCC	2937
Db	1798	CATGCTTATACCCCTGGCTGCTTACGCCCTGGATCCCTCACTGCCACCGTACTATTTGAT	1857	QY	2524	GCCTGCAAGGGACAGGACTTCAGCTGCGGCGCACACTGGCTCTGGCTCACCTC	2583
Qy	1576	GATGACCATGAGGCACTTCACTTTGAAATGAGTACTATTCATGTCAGTGGAGCATT	1635	Db	2938	GCGCCANGGGAACAGTCAGTGTGCCCCGGCACTGGCTCTGGCTGAGCTTCTGTCACHTC	2997
Db	1858	GATGACCATGCTGCATCTTACTTTGAGAACCGTACTATGAGTGGAGCATT	1917	QY	2554	TTCACCACTTTCATGTCATGAGCTGCGGCTCTGAGCGAGGGCACACTGGCTCTGGCTCACCTC	2643
Qy	1636	GGGTTATGGAGSTCAGGTCGGGACAGCCAAAGGGGGTACAGTCATGTCCTCC	1695	Db	2998	TTCACCAATTTCATGTCATGAGCTGCGGCTCTGAGCGAGGGCACACTGGCTCTGGCTCACCTC	3057
Db	1918	GGCATCATGGAGGGAGARAGTCTGAGAACATCCTGGAGCACGAGCTGGAAATGTTCTGTTCC	1977	QY	2644	GGAGGGGACTTGTGGCCCTGGCTGCAAGCTGCCACACATGGCTCTTGAGAG	2703
Qy	1696	TTAGGAGCTAGGAGGGACAGCCAAAGGGGGTACAGTCATGTCCTCC	1755	Db	3058	GGAGGTAGCTGGTGGGCCGGACGTGCCAAGTCTCCATCTCTGCGCTC	3117
Db	1978	TATGACCATGAGGGACGCCAGGGTGGAGGACTTGAGGACATGGCTGAGGACATGCGGA	2037	QY	2704	CTGGGCTCTCATACATCTCTGCAACACTAGAGGCTTATGTCATCATCAGGGTT	2763
Y	1816	GAGGAATNCGAAGGCAAGAGAAATTCATGTCCTTGGGACCGAAATGATGGATG	1873	Db	3118	CTGGGCTCTGACATTCTCTCCCTGGAGGCCTACTGCCACATAAAGGCTC	3177
Db	2098	GAGGAGTATGAGAGAAAACAGACCTTCCTGGATGGAGAGCCCGCTGGTGGAG	2157	QY	2764	TAA	2766
Qy	1874	-----	-----	Db	3178	TAA	3180
Db	2158	ATGAGTGAGAAGAACCCCTGTTATGAGCTGTTGCTTCACAATACAGGAA	2217	RESULT	7		
Qy	1883	TATCAGATGTGACAGACG-----	1901	ABV24305			
Db	2218	TACTGTATGGCCAGCTGTCCTCAGGAAGTCTATGCTAGAGAACATCCACTCCCTC	2277	ID	ABV24305	standard	cDNA: 5438 BP.
Qy	1902	-----	-----	XX	AC		
Db	2278	ACTATAATCACCAGCAGATGATGACAGCAAGCAGCCACTGACCAAGAG	2337	XX	XX		
Qy	1924	GGGCCAAGGAGTACCGAGAGATGGGAAGGCGATTTGGGACACCCAACTGAGA	1983	DT	ABV24305;		
Db	2338	GAAGAGAGGCATTTGGGAAATGGGCCCACTCTGGAGACACAGCAGCTGGAG	2397	XX	DE	Human prostate expression marker cDNA 24296.	
Qy	1984	GCGATCATGAGAGCTATGAGTAAAGTACCGTGGACAAACGTACATGAGAGA	2043	XX	KW	Human; prostate cancer; cryostatic; carcinogen; pharmacodynamic marker;	
Db	2398	GTGATCATGAGAACTTACAGGTCAGAGTACCGTGGACAAACGTAGTAAAGAGCA	2457	XX	KW	Pharmacogenomic marker; gene; ss.	
Qy	2044	AACCTGGCTTGTGGGGACCCATTCCGGAGGACCTATGGGACACCCAACTGAGA	2103	XX	OS	Homo sapiens.	
Db	2458	AACTTAGCCCTGTGGGGACGAGACAGCTGGAGAGACAGTCACTGGAGGCA	2517	XX	PN	WO20160860-A2.	
Qy	2104	GTCTAGTCAGGGATGGATGAGGATGATCCGGGGAGGGCTGCCCTCTGC	2163	PD			
Db	2518	GTGAGTGTGGGGAGATGACCTGGAGGAGCTGGAGGAGACGCTGCCCTCTG	2577	XX	PD	23-AUG-2001.	
Qy	2164	TTCGACTACGTCAGGACTTCGTACTGCTCTGGAGGGCTGGCTGGGCC	2223	XX	PF	20-FEB-2001; 2001WO-US05171.	
Db	2578	TTTGACTACGTCAGTGTGACTTCGTGCTGGCTGGAGGTCTGCCCC	2637	XX	PR	17-FEB-2000; 2000US-183319P.	
Qy	2224	CCACACAGTACTGCGACGGCTGCTGGCTCTGCTCATCTCATCATGTCATG	2283	PR	16-MAR-2000; 2000US-189862P.		
Db	2538	CCGACAGAGTACTGGACAGGGCTGGCTCATCTCATCATGTCATGCGCTA	2697	PR	25-MAY-2000; 2000US-207454P.		
Qy	2344	TGACTGAGCTGTTGGGAGCTGGGCTGGCTGCTGGCTGCTGGCTGCTGG	2403	PR	09-JUN-2000; 2000US-211314P.		
Db	2284	CTGACCCCATTTGGGACTTGGCTCGACTTGGCTGCCATTGGCTCAAGAT	2343	PR	18-JUL-2000; 2000US-219007P.		
Db	2698	CTGACGGCTTCTGCTGACACTTCGGCTGCCACATCGCGCTGAGGAT	2757	PR	13-DEC-2000; 2000US-255281P.		
Qy				XX	PA	(MILL-) MILLENIUM PREDICTIVE MEDICINE INC.	
Db				XX	PI	Schlegel R, Endege WO, Monahan JE;	
Qy				XX	DR	WPI; 2001-662795/76.	
Db				XX	PS	Claim 1; Page 4554-4555; 11750pp; English.	
Qy				XX	PT	The invention relates to an isolated nucleic acid molecule (1) comprising	
Db				CC	PT	a nucleotide sequence given in Tables 1-9 (A00010-AB62213) of the	
Qy				CC	PT	specification or its complement. (1) is useful for:	
Db				CC	PT	(a) assessing whether a patient is afflicted with prostate cancer;	
Qy				CC	PT	(b) monitoring the progression of prostate cancer in a patient;	
Db				CC	PT	(c) assessing the efficacy of a test compound to inhibit prostate	
				CC		cancer in a patient;	

(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

(e) selecting a composition for inhibiting prostate cancer in a patient;

(f) assessing the prostate cell carcinogenic potential of a compound;

(g) determining whether prostate cancer has metastasized in a patient;

(h) assessing the aggressiveness or indolence of prostate cancer in a patient;

(i) is also useful as a pharmacodynamic or pharmacogenomic marker.

Db	982	CCAGAGAGGACTTAGTCAGCTGGAGAAATGCCCTAGGATTCGCTTCCACCA	1041
Db	1145	CCAGATAGAAATAGACGAAATTAGATAGATTAGCTAACCTACGAGCTCTAAGCAG	1204
Qy	1042	CAGAGAGCCGCCCTTACCTATCAGCAAGCCACTCGTATGATGACTGTTGGCAGA	1101
Db	1205	ATCCTGAGAACATGAGCAGAGCAAGCCACTCGTATGATGACTGTTGGCAGA	1264
Qy	1102	ATCCTGAGAACATGAGCAGAGCAAGCCACTCGTATGATGACTGTTGGCAGA	1161
Db	1265	ATTTAAAGAGGATGAGCTGACCAAGGAGGCTGAGCTGAGCTGAGCTGAGCTGAC	1324
Qy	1162	ACCGATGAGCTG---AGGACTTATTCGACGGCTTGTGACCCATGTTCTACAG	1218
Db	1325	ACTGAAGTGAATGAAATGACCGCTGTTAGTAAGTCTCTTGTGAGAACAGGA	1384
Qy	1219	TGCTGGAGAACITGGCTGACTCTCCCTGACAGTGGTGAAGAAAGGGAGACAT	1278
Qy	1279	AGGACCAAGTGTGGACTACAAACAGAGGAGGTTGCGCAATGCGAGGGTCA	1338
Db	1385	TGCTGGAGAACITGGCTGACCTTATCCGAGGGTGTGATGACT	1444
Qy	1445	AACTACTGTTGTTGACTCTCAGACAGGAGGTCACAGCAATGCTGGCTGAT	1504
Db	1459	GACTCACAGAGGCACGGGGTCTGAGCCAGGAGGACCCAGAGGACTCTCCG	1398
Qy	1399	GSCATAATGATGACGACATTGAGGGAGTACACCTCTCTGTAAGGTTGAGCA	1458
Db	1565	GGTATCATGATGATGATCTTGAGGGAGTAAATTCCTGTGATCTCAGCAAT	1624
Db	1579	GTCGCGATAGAGGAGCACCCAGGAGGGGGATGCCCTCACAAATTCACAGCT	1518
Db	1625	GTCAGAAGTACTCTGTGAGCTTGAAGAATGGCTACTGAGCAATGCTGAT	1675
Qy	1519	CCCTGCGCTCGGGTGTCTAGCCTCCCTGTGTCGCGACAGTTACCTCTGGAT	1578
Db	1676	GTTCCTACACTCTCTGCTCCGGATCCTCCACTGCGACTGTAATTTGTGAT	1735
Qy	1736	GACCAAGGGCGATTTTACTTTGAGGACCTGTGACTCATGTGAGGATGTC	1795
Db	1769	GATCATGGGGTCAAGTTCTGGCACATCAGGTCGCCGGTACAGTCATGTCCTT	1698
Db	1856	ATCAGGGGTGAAGTTGTGACATGGGGGGGGATTTGAGGACATGTGTCAT	1855
Qy	1699	AGCACAGTAGAGGGACGCCAACGGTGGGGTAGGACTTGTGAGACATATGGAG	1758
Db	1856	AAACACATCGAGGGCTCCAGGGTGGGGGGGGATTTGAGGACATGTGTCAT	1915
Qy	1759	TGGAATTCAGATGAACTGTGAAACCTAAGGTTAAATAGATGAGGAG	1818
Db	1916	CTCGAAATTCCAGATGATGAAATGTCAGAACAAATTCAGTCAGGAAATGAG	1975
Qy	1819	GTATACGAAAGGAGAGGATTCCTCATGCCCTGGACCGGAATGGATGAA	1875
Db	1976	GAGTATGGAGAACAGACCTCTTCCCTGATGAGGAGGAGGAGGAGGAG	2035
Qy	1876	-----	1875
Db	2036	AGTGAGAGAACGCCCTATGATGAGCTTGGGCTCACAAATACAGGAAATAC	2095
Qy	1876	-----	1875
Db	2096	CTGTTGGCCAACCTGCTCTCAGGAAGGTCTAGAACATCCGATCTCTACT	2155
Qy	1876	-----	1926
Db	2156	GTAACTCACCATTGAGGAAATGATGCAAGCAGGCCCTGAGCCAGGAGGAG	2215

QY	1927	CCANAGAGGATACAGAGATGGAAAGCCAGTATGGGAAACCCCCAACATGAACTC	1986	PN
Db	2216	GAGAGGCAGCATGGAGAAATGGGGCCCATCTGGGAGAGCACCHAGTGGAGTG	2275	XX
Db	1987	ATCAATGAAAGAGTCTATAGTCAAGACTACGGTGGACAACTGATGAGAAC	2046	PD
Db	2275	ATCAATGAAAGAGTCTATAGTCAAGACTACGGTGGACAACTGATGAGAAC	2335	11-OCT-2001.
QY	2047	CTGGCCCTGTTGGGGGGGACATTCCTGGAGGACCATCTGGAGGAGAC	2106	XX
Db	2336	CTGGCCCTGTTGGGGGGGACATTCCTGGAGGAGAC	2395	XX
QY	2107	AGTCGAGCGGGGGAGGATGAGGATGATGAGGAGATCGGGAGGAGGAGCT	2166	PR
Db	2396	AGTCGAGCGGGGGAGGATGAGGATGATGAGGAGATCGGGAGGAGGAGCT	2455	PR
QY	2167	GACTAGTGTATGCACTTCTGACTGTCGTTGGAGGAGCTGTTGGAGGAGCT	2226	PR
Db	2455	GATTCGTTATGCACTTCTGACTGTCGTTGGAGGAGCTGTTGGAGGAGCT	2315	PR
QY	2227	ACAGAGTACTGCCACGGCGCGCTGCTTGGCCCTCTCATCCATCATGTCATG	2286	XX
Db	2516	ACTGAACTACTGGAAATGGCTGGCGCTGGCTCATGTCATGATGGCCATAC	2575	XX
QY	2287	ACCCGATATTGGGAGACCTGGCTCCACCTTGCTGACCATGGCTCAAGATCA	2346	CC
Db	2576	ACACCTTCATTGGAGACCTGGCTCCACCTTGCTGACCATGGCTCAAGATCA	2335	CC
QY	2347	GTCAACAGCTTGTGTTGGCTGGCAATGGTCCACCTTGCTGACCATGGCTCA	2406	CC
Db	2635	GTGACTGCACTGCTGCTGCACTGGACATAGTCAGACAGACATGGCAGCA	2695	CC
QY	2407	GTCTCTGCTCCAGGATCTATAGCAGCGCCATGGCACTGGCTGGGGAGAAC	2466	CC
Db	2696	GTGGCAGCACCCAGGACAGTACAGTCAGACGGCTCATAGTAACGTCAGGCA	2755	CC
QY	2467	GGCTCAATCTCTGGCATGGCTGGCTGGGGGCACTATGGG	2326	CC
Db	2755	GGCTCAATCTCTGGCATGGCTGGGGGCACTATGGG	2815	CC
QY	2527	CTGCAAGGAGCAGGAGTTCACGTCGTCGGGGCACTGGCTTCTCCACCTCTC	2586	CC
Db	2815	GCCATGGGACAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGGCA	2875	CC
QY	2587	ACCATCTTGCAATGTCGCAATCAGCGGCTCTGTACCGAAGGGCGCACCTGG	2646	CC
Db	2876	ACCATCTTGCAATGTCGCAATCAGCGGCTCTGTACCGAAGGGCGCACCTGG	2935	CC
QY	2647	GGGAGCTGGCTGGCCCTGGGACACCGACATGGCTTGAGGAGCTGGTGGACCTG	2706	CC
Db	2935	GGGAGCTGGCTGGCCCTGGGACACCGACATGGCTTGAGGAGCTGGTGGACCTG	2995	CC
QY	2707	TGGCTCTTACATCACTCTTGCAACACTAGASGCCATTGTCTACATCAAGGGTCTCA	2766	CC
Db	2996	TGGCTCTTACATCACTCTTGCAACACTAGASGCCATTGTCTACATCAAGGGTCTCA	3055	CC
RESULT	8			
AA\$0968	AA\$0968	standard; cDNA: 1187 BP.		
AC	AA\$0968;			
DT	13-FEB-2002 (first entry)			
DE	DNA encoding novel human diagnostic protein #26772.			
XX	Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss. Homo sapiens.			
XX				

Db 493 CCTGGAGGGACCACTCATGGGGCATCACCGTCAGTGAGCAGGGATGAGGATGAGG 552 PR 04-OCT-2000; 2000GB-0024263.
 Qy 2132 ATGAATCCGGGAGSAGAGCTGCTGCTCTCGCTGCTGCTGACTGACTTCCTGACTG 2191 XX
 Db 553 ATGAATCCGGGAGSAGAGCTGCTGCTCTCGCTGCTGCTGACTGACTTCCTGACTG XX
 Qy 2192 TCTTCTGGAGGTGCTGTTGCCCTGTGCCCCCACAGACTGCCCACGGCT 2251 XX
 Db 613 TCTTCTGGAGGTGCTGTTGCCCTGTGCCCCCACAGACTGCCCACGGCT 612 XX
 Qy 2252 GCTTCTGGCGCTCCATCCTCATCATGGCAGCTGCCCCCACAGACTGCCCACGGCT 2311 XX
 Db 673 GCTTCTGGCGCTCCATCCTCATCATGGCAGCTGCCCACGGCT 732 DR
 Qy 2312 CGCACTTCGCGTGCACCATGGTCMAAGATCAGTCACAGCAGCTGTTGCGCAT 2371 XX
 Db 733 CGCACTTCGCGTGCACCATGGTCMAAGATCAGTCACAGCAGCTGTTGCGCAT 792 PT
 Qy 2372 TTGGCACCTCTGTCGCCAGATAGCTGTTGCCAGCCAACTGCTGCCCCTCAGGATATAG 2431 XX
 Db 793 TTGGCACCTCTGTCGCCAGATAGCTGTTGCCAGCCAAAGCTGCTGCCCTCAGGATATAG 852 PT
 Qy 2432 CAGAGCCCTCATTCGCAAGTGTAGGGCAGCAAGCCGCATATGCTCTCTGSCATCG 2491 XX
 Db 853 CAGAGCCCTCATTCGCAAGTGTAGGGCAGCAAGCCGCATATGCTCTCTGSCATCG 912 PS
 Qy 2492 GCTCTGGCCCTGTCCTGGCGCCTACGGCCTGCTGAGGAGTTCACTGCT 2551 XX
 Db 913 GCTCTGGCCCTGTCCTGGCGCCTACGGCCTGCTGAGGAGTTCACTGCT 972 Claim 4; SEQ ID NO 12785; 639pp + sequence listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for
 CC measuring human gene expression in a sample derived from human foetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC fetal liver. The present sequence is a single exon nucleic acid
 CC probe of the invention.
 Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct/sequences.
 XX
 Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other;
 Query Match 28.5%; Score 787.2; DB 22; Length 1836;
 Best Local Similarity 68.3%; Pred. No. 3.9e-16; Mismatches 503; Indels 39; Gaps 4;
 Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4;
 Qy 109 GACGTGCCAACACAGGGCAGAACATGAGCCTGTCAGGTCAGCAGGAG 158 XX
 Db 133 GAATGGAGGAGAAGGAATGAGTGAATGTTACTGGATCATATTACTGTAGAA 192 XX
 Qy 169 GGTGTGATCCGCCAACCTGGTACCGGGAGACCCCTCCCTGGGACACAGATGGCAGG 228 XX
 Db 193 GGGGATATTGGCCATTGGAACCCAGACCCCTTGGGACAAATTGCGTGA 252 XX
 Qy 229 GTCATGTCATATTGGCCCTGATATACATGTTCTTGGGTGTCATCATGGTAC 288 XX
 Db 253 GCTACTGIGTATTGTCGCAATGGTCTACATGTTCTGGAGTCATAGTGTAT 312 XX
 Qy 289 CGCTTCATGGCATCATTTGAGTCATCACCCCTCAAGAGGGAGTGACAATTAGAA 348 XX
 Db 313 CGGTTCATGTCCTCTATAGAAGTCATCACCTCAAGAAAGAAATACATAAGAA 372 XX
 Qy 349 CCCATGGAGAACGCCAACCAACCAATTGGCTGTGATGAATGACTGTCACCTG 408 XX
 Db 373 CCCAATGGAGAACGCCAACCAACCAATTGGCTGTGATGAATGACTGTCACCTG 432 XX
 Qy 409 ACCCTTATGGCCCTGGTTCTCTGCTCTGAGATACTCCCTCTTAATGAGGTTG 468 XX
 Db 433 ACCTGATGGCCCTGGGATCTCTGCTCTGAGATCTCTTCACTAATGAGTGT 492 XX
 DT 01-FEB-2002 (first entry)
 DE Human foetal liver single exon nucleic acid probe #12785.
 XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
 KW XX
 OS Homo sapiens.
 XX
 PN WO200157277-A2.
 PR 09-AUG-2001.
 XX
 PR 30-JAN-2001; 2001WO-US000669.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207456.
 PR 30-JUN-2000; 2000US-060808.
 PR 03-AUG-2000; 2000US-062366.
 PR 21-SEP-2000; 2000US-0236687.
 PR 27-SEP-2000; 2000US-0236359.

QY	769	TTCCTACAAATACATGCCACAAAAGTACCCACAGACAAACCCGAGGAATTATCATAGAG	828	RESULT 10
Db	793	TTTACAAATACATGCCACAAAAGTACCCACAGACAAACCCGAGGAATTATCATAGAG	852	ABA31619
QY	829	ACAGAGGGGACACCC-----TAAGGGCATGGAGATGGGGAAATATGAA	879	ID ABA31619 standard; DNA; 1836 BP.
Db	853	CATGGAGGACAGGCCATCTCTAACAGAGGTATCCAGCTGGCAAGCAGGGGATGATATGAA	912	XX
QY	880	TCCCATTTCTAGATGGGACCTGGTGCCTGGAGGGAG	921	XX
Db	913	TCTCATGTTGAAATTCTCTAGAATGGTGGCTGGAGGAAAT	972	DT 23-JAN-2002 (first entry)
QY	922	GAAGTGTAGTGTGAGAGAGATGGAGATGGGGAG-----	981	XX
QY	973	GATGATGAGAAGCTAGGGAGAATGGTAGGATCTGAGTCTGAGGAACTTACAGAGCAT	1032	DE Probe #10085 for gene expression analysis in human heart cell sample.
QY	982	CCAGAGAAGACTTAGATAGCTGTGGAGATGCCAAATACTATGCTTTTCCACCAA	1041	KW Human: gene expression: heart; microarray; vascular system; probe;
Db	1033	CCACATAAGAAATAGACATTATAGATAATGATTAACCTACCAAGTCCAGTCAGCAG	1092	KW cardiovascular disease; hypertension; cardiac arrhythmia;
QY	1042	CAGAGAGCCGCCCTCACCGTATCCAGCCACTCGATGACTGTCAGGAGCAAC	1101	KW congenital heart disease; ss.
Db	1083	CAAAAGATGAGGATTATCGATTCAGCTACTCGCTCAGTGTGCAAC	1152	OS Homo sapiens.
QY	1102	ATCCATGAGAACATGAGCAGAACAGGCAAGAAGGCTTCAGATGAGCTGAGGCAAC	1161	XX
Db	1153	ATTTAAAGAGGCTGAGCTGAGCAAGGAGGCTGTCAGATGAGGTCAC	1212	PN WO20157274-A2.
QY	1162	ACCGATGACCTG--AGGACTTATTCAGGCTTGTGACCTTGACCTTGAC	1218	XX
Db	1213	ACTGAGTACTGAAATGACCCCTGACTAAGCTCTGACACAGGACATACAG	1272	PD 09-AUG-2001.
QY	1219	TGCCCTGGAGAACCTGGCTACTCCAGTGGTCAAGGAGGAGCATGTC	1278	XX
Db	1273	TGTTGAGAACCTGGTACTGGCCCTTACCAATTACCGACAGGTGATGACT	1332	PF 30-JAN-2001: 2001WO-US00666.
QY	1279	AAGACCATGATGTGGACTACAAACAGGGATGTTCTCCAAATGCAAGGGCTACTAT	1338	PR 04-FEB-2000: 2000US-0180312.
Db	1333	AACACTGTGTTGTGACTTCAGACAGGAGATGGCTGAGGACAT	1392	PR 26-MAY-2000: 2000US-0207456.
QY	1339	GAGTCACAGGGCACGTGGTCTGAGCCAGGAGAACCCAGAGGAGTTCGGTG	1398	PR 30-JUN-2000: 2000US-0608408.
Db	1393	GAATTTACTGAGGACTCTGGTTAAACCTGTGATGAAATCAGAGTG	1452	PR 03-AUG-2000: 2000US-0632365.
QY	1399	GGCTTAATGTGAGCACCTTGGAGGATGACACTCTTGTAAAGTTGAGCAAT	1458	PR 21-SEP-2000: 2000US-0234687.
Db	1483	GGTATCATGATGATGATCTTGTGAGGGGATGAAATTCCCTGTGATCAGCAAT	1512	PR 27-SEP-2000: 2000US-0236359.
QY	1459	GTCGCATGAGGAGGCCAGGGGGATGCCCCAGAAATATCAACAGTC	1518	PR 04-OCT-2000: 2000US-0024263.
Db	1513	GTCAAAGTACTCTGAGCTCAGAAGATGGCAATCTGGAAAGC-----	1563	PA (MOLE-) MOLECULAR DYNAMICS INC.
QY	1519	CCCTTGCCCGGGCTGTCTAGCCTCCCTGGCTGGGACAGTACCTCTGGATGAT	1578	XX
Db	1564	GTTCTACACTCTGCTGGATCTCCCTCCACTGCTGACTGATGAT	1623	XX
QY	1579	GACCATGAGGCACTCTCACTTTGATGATCATGTCAGTGTAGATGAT	1638	PT Single exon nucleic acid probes for analyzing gene expression in human hearts -
Db	1624	GACCACTGGCATTTTACTTGTGAGGACCTGACTCATGTCAGTGTAGCATG	1683	XX
QY	1639	GTTATGGAGGCTCAAGGTCTGGGACATGGTCCCGCGGTACAGTCATGTCCTG	1698	PT
Db	1684	ATCATGGAGGCTGAAAGTATGAGACATCTGGAGCTCGAGGAATGTTACGATAT	1743	PI Penn SG, Hanelz DK, Chen W, Rank DR;
QY	1699	AGGAGGAGAACGCCAACGGTGGCTGAGGACTCTGACTCATGTCAGTGTAGCATG	1758	XX
Db	1744	AAACACATGAGGCACTGCTGAGGAGGCTGAGGAGGAGGAGGAGGAGGAGGAG	1803	PS Claim 4; SEQ ID No 10085; 530PP; English.
QY	1759	TGGAATGAGAATGATGAACTGTGAA	1788	XX
Db	1804	CTCGAAATCCAGATGAGGAAATGTGAA	1833	XX
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other; SQ				
Query Match 28.5%; Score 787.2; DB 22; Length 1836; Best Local Similarity 68.3%; Pred. No. 3e-216; Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4; XX				
Sequence 1836 BP; 512 A; 336 C; 464 G; 524				

QY	349	CCCAATGGAAACCAAGCAGAACCACTATTGGGTTGGAAATGTCCTCAACACTG	408	1399 GGCATTAATGATGAGCACATTGAGGAGGATGACACTCTTGTAAAGTTGAGCAAT	1458
Db	373	CCCAATGGAAACCAAGCAGAACCACTATTGGGTTGGAAATGTCCTCAACACTG	432	1453 GGATCATAGATGATGATATCTTGAGGAGGATGAAATTCTCTGTGCACTCAGCAAT	1512
QY	409	ACCCATATGGCCCTGGTTCTGTCGTCAGATACCTCTCTTAACTGGAGGTTG	468	1459 GTCGCATAGAGGGAGGCCAGAGGGGGGCCCTCCAGCAATATCACAGCTT	1518
Db	433	ACCTTGATGCGCCCTGGATCTCTGTCCTCAGATGATCTCTTCAAGTAAGGTTG	492	1513 GTCAAAGTATCTCTGAACTCTTCAGAAGATGGCATACTSGAAC-----CAT	1563
QY	469	GGTCATGGGTCATGCTGSGATCTGGGACTCTTCACTATGAGGAGGCTTC	528	1519 CCCTGCCCTGGGCTAGGCCTCCCTGTGTCAGCAGTACCATCTGGATG	1578
Db	553	AATATGTCATCATATTGACTCTGCTGTCAGGAGAACAGCAAGG	612	1624 GACCAAGCAGGATTTACTTTCAGGACCTGTCAGCTGAGCAATGTCG	1683
QY	589	ATCAGACATCAGGACTCTCATCACCCTGCTGGAGATCTTGTGCTACATG	648	1639 GTCATGGAGGTCAGGTTGCGGACATCGGTGCCGGTAGTCATGTCCTT	1698
Db	613	ATTAGCATATGCGTCCTCTTGTGACAGCAGCTGGAGCATCTGCCAACCTGG	672	1684 ATCATGGAGGTAATGACATTCATGGACATCTGTCAGTGTGAGCAATGG	1743
QY	649	CTCTATATGATCTGCGAGCTCTCCCTGGCTGGAGGAGGCTCTC	708	1699 AGGAGTAGAGGACGCCAAGGGTGGGGTAGCTGAGACATATGGG	1758
Db	673	CTTACATTATTTGTGTCATATCTCTCTGGTGTGAGGCTCTG	732	1744 AACACATCGAGGGACTGCGCACAGGGGGATTTGAGGACACTTGAGG	1803
QY	709	ACTCTCTCTTCCAGCTGTCCTCTGGCTGGAGAGAACACTGCTC	768	1759 TTGGAATTAGAATGATGAACTGTGAA	1788
Db	733	ACTCTCTCTTCCACACTGTCGTGTCGTGTCGTGAGGATGAGACTCTG	792	1804 CTCGATTCAGAATGATGAATTTGTAA	1833
QY	769	TTCTACAAATACATGACAAAGTACCGACAGAACACCGAGAAATACATGAG	828	RESULT 11	
Db	793	TTTACAGATGTCATCACAGGGATCGAGCTGGCACAGAGGGGATGATTATGA	852	AAK12937	
QY	829	ACAGAGGTTACCAACCC-----TAAGGCATATGAGATGGATGGAAATGAAAT	879	AAK12937 standard; DNA; 1836 BP.	
Db	853	CATGAGGAGAACAGGCATCTTAAGACTGAATGAAATGGGGAAATGGTCAAT	912	XX	
QY	880	TCCCATTTCTAGATGGAACCTGGTGTCCCCCTGGAAAGGGAG-----	921	DE Human brain expressed single exon probe SEQ ID NO: 12928.	
Db	913	TCTCAGTGTAAATTCTAGATGGTGTGTCGGGGATGAGGGACCA	972	AC	
QY	922	GAAGTGGATGAGTCCCGCAAGAGAGATCGGGATCTCAAGATGAGCAAAAC	981	XX	
Db	973	GATGATGAGAAGACTAGGGAGRAATGGCTAGGAGACTTAAGGAGAACAT	1032	KW Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer; ss.	
QY	982	CCAGAGAAGACTTAGATCCTGGGGAGATGCCAATTAATCTATGCTCTTCCRCAA	1041	XX	
Db	1033	CCAGATAAGAAATAGCAATTATGAGATTAGCTRACTACCAAGTCTTAAGTCAGCAG	1092	OS Homo sapiens.	
QY	1042	CAGAAGGCCGCCCTCTACCGTATCCAAGCCACTCTGATGATGTCAGGAAAT	1101	XX	
Db	1093	CAAAAAGTAGCATTTATGCACTACTGCTCATGACTGGCTGGCAC	1152	PN WO2001575-A2.	
QY	1102	ATCCCTAAGAACATCGAGCAGAACAGCAGAACAGAGGCTCCAGCATGAGGAGGCA	1161	XX	
Db	1153	ATTTAAGAGGCGATGCACTGAGCTGACCATGAGGCTGGCAC	1212	PR 04-FEB-2000; 2000US-0180312.	
QY	1162	ACCGTGTGAGCT---AGGACTTTATTCAGGTCTCTTGACCCATGTTTACAG	1218	PR 26-MAY-2000; 2000US-020456.	
Db	1213	ACTGAAGTGTACTGAAATGACCCCTGTAGTAAATGATCTTGTGACAGGGACATATCG	1272	PR 30-JUN-2000; 2000US-060408.	
QY	1219	TGCCCTGGAGACTGTGGGGTGTACTCTCTGAGCTGAGAAGGGAGACATGTC	1278	PR 03-AUG-2000; 2000US-053256.	
Db	1273	TGCTCTGGAGACTGTGGTACTCTGGCCCTTACCATATTCGGAGAGGTGGGATGACT	1332	PR 21-SEP-2000; 2000US-0234687.	
QY	1279	AAGACCATGTTGTTGTTGACTACAAAGAGGAGTGTCTGCAAGCTGCTGAGT	1338	PR 27-SEP-2000; 2000US-0236359.	
Db	1333	ACACATGTGTTGTTGACTACAAAGAGGAGTGTCTGCAAGCTGCTGAGT	1392	PR 04-OCT-2000; 2000US-024263.	
QY	1339	GAGTCACAGAGGGCAGGGTCTGACAGCAGGAGGACCCAGAGGAGTCTCGT	1398	XX	
PA		(MOLE-) MOLECULAR DYNAMICS INC.		PA Single exon nucleic acid probes for analyzing gene expression in human brains -	
PI		Penn SG, Hanzel DK, Chen W, Rank DR;		PI; 2001-48346/52.	
XX		Example 4; SEQ ID NO: 12928; 650pp + Sequence Listing; English.		XX	
CC		The present invention provides a number of single exon nucleic acid		CC	

XX	589	ATCAACGCTACAGACTCTCTCATCACGCCCTGCTGAGATCTTGTGCTACATCTGG	QY
PD	09-AUG-2001.		QY
XX	613	ATTAGCTTGGGCTCTCTTGTGACAGCAGCTGAGACATTTGCTACCTGG	Db
PF	30-JAN-2001; 2001W0-US005670.		QY
XX	649	CTCTATATGATCTGCGAGCTCTTCGCCCTGGTGGTCCAGGTGTTGGGAGGGCTCTC	Db
PR	04-FEB-2000; 2000US-0180312.		QY
PR	26-MAY-2000; 2000US-0201456.		Db
PR	30-JUN-2000; 2000US-0608408.		QY
PR	03-AUG-2000; 2000US-0632366.		Db
PR	21-SEP-2000; 2000US-0234987.		QY
PR	27-SEP-2000; 2000US-0236559.		Db
PR	04-OCT-2000; 2000GB-0024263.		QY
XX	769	TTCTACATATTGCTGCTGCTATCTCCCTCTCTGGTGGAGGTCTGGAGGGTTGCT	Db
PA	(MOLE-) MOLECULAR DYNAMICS INC.		QY
PI	Penn SG, Hanzel DK, Chen W, Rank DR;		Db
XX	WPI; 2001-488901/53.		QY
XX	Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells -		Db
PS	Claim 25; SEQ ID No 9397; 487pp; English.		QY
XX	The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.		Db
CC	Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct/sequences .		QY
CC	Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other;		Db
CC	Query Match 28.5%; Score 78.7; DB 22; Length 1836;		QY
CC	Best Local Similarity 68.3%; Pred. No. 3. 9e-16; Mismatches 503; Indels 39; Gaps 4;		Db
Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4;	QY	922 GAAGTGGATGACTCCGGCAGAGAGATGATCCGGATCTCAAGATCTGAGCAAAAC	QY
QY	109 GACGTCGCAAGCAGGGCAGAACATGACTCTGTCAGGGCATCGGACTGCAAGGAG	981	Db
Db	133 GAAATGGAAGGAGAAAGAATGAACTGGAACCTGTTGATGATGTTGATGAAAGAA	973	Db
QY	169 GGTGTCATCCGCCAACCTGGTACCCGGAGAACCTTCCCTGGGCAAGATGTCAG	973	Db
Db	193 GGGGATTGTCGCCATTGGGACCCAGACCCCTTGGGACAAATTGCTA	973	Db
QY	229 GTCATGTCATTGTCGCTGAAATACATGTTCTGGGTGTCATGATGTCAG	1102	Db
Db	253 GCTACTGTCATTGTCGCTGCAAGCTTCTGGAATCTAGCTGATGTCAG	1102	Db
QY	289 CGCTTCATGSCATCTATGAACTGTCACCCCTCAAGAGGGAGTGACATTGAA	1102	Db
Db	313 CGGTTCATGTCCTCTATAGAATGTCATCACATCTCAAGAAAGAAATAACCTAAAGAA	1102	Db
QY	349 CCAATGAGAACAGCACACCACTATGGGCTGGATGAACATGCTCCACCTG	1102	Db
Db	373 CCAATGGAGAACCCAGCAACAGAACACTGTCAGGAGTGACATTGAA	1102	Db
QY	409 ACCCTTATGGCCCTGGTTCTCTGCTCTGAGATACTCCCTCTTAATGAGGTGT	1102	Db
Db	433 ACTTGATGGCCCTGGATCTCTGCTCTGAGATCTCCCTCTGAACTAATGAGGTGT	1102	Db
QY	469 GCTCAGGGTCAATGCTGGTGTACGGGACCTTACCAATGTCAGGAGTGACCTC	1102	Db
Db	493 GCCCATACTCCTGAGGAGACCTGGTCCTAGCACCATGTCGATCATTGCT	1102	Db
QY	529 AACATGTCATCATGTCGCTGTCAGTGTGCTGAGATGAGCTGGCAAG	1102	Db
Db	553 AATATGTCATCATGTCGCTGTCAGTGTGCTGAGGAGACAGGAAG	1102	Db
QY	589 ATCAACGCTACAGACTCTCTCATCACGCCCTGCTGAGATCTTGTGCTACATCTGG	1102	Db
Db	613 ATTAGCTTGGGCTCTCTTGTGACAGCAGCTGAGACATTTGCTACCTGG	1102	Db
QY	649 CTCTATATGATCTGCGAGCTCTTCGCCCTGGTGGTCCAGGTGTTGGGAGGGCTCTC	1102	Db
Db	673 CTTACATATTGCTGCTGCTATCTCCCTCTCTGGTGGAGGTCTGGAGGGTTGCT	1102	Db
QY	709 ACTCTTCTCTTCACTGCTGTCGTCCTGGCTGGCTGGAGATAACGATGTC	1102	Db
Db	733 ACTTCTCTCTCTTCCACATCTGCTGTCGTCAGGATAGGAGACTCTG	1102	Db
QY	769 TTCTACAAATCATGACAAAAGTACCCGACAGACAAACGGAGATTATGAGA	1102	Db
Db	793 TTTCAGAGTGTCTACAGAGGATTCAGCTGCTGGCTGGAGGGATGCTT	1102	Db
QY	829 ACAGAGGGTGAACCC-----TAAGCTGATGAGATGGATGGAAATGATA	1102	Db
Db	853 CATGAGGAGAGCCATCTCTAGACTCTAACATGAGTGGAGGGAAATGTCAG	1102	Db
QY	880 TCCCATTTCTCPAGATGGACCTGCTGGCCCTGGAGGGAGGGATGCTT	1102	Db
Db	913 TCTCAGTGTGAATTTCTTGTAGATGGTGTCTGGCTGGTGTGAGGGATGAGG	1102	Db
QY	922 GAAGTGGATGACTCCGGCAGAGAGATGATCCGGATCTCAAGATCTGAGCAAAAC	1102	Db
Db	973 GATGTAAGAGCTGGGAGAACTGCTAGGCTAGATGTTGAGAACTTAAGCAGAC	1102	Db
QY	982 CCAGAGGGACTTACATCTACACTGGGAGAGTGGAGATGGCCAAATRACTANGCT	1102	Db
Db	103 CGCAGATAGAAATAGAGCAATTAAATGAAATAGATGACTACCAACTCTGAG	1102	Db
QY	1042 CAGAGAGCCGCCCTCTACCGTATCCACGCCACTGTGATGATGACTGGCAGCA	1102	Db
Db	1093 CAAAATGAGCATTTATGCACTCACCTACGCTACTCGCTCATGAGCTGGCAC	1102	Db
QY	1102 ATCTGAGAAACATGCGACACAGCCAGAGGCCCTCAGCATGAGGGGGCC	1102	Db
Db	1153 ATTTAAAGAGCTGCGACGCGTACGGAGAACTGCTGAGCTGAGGAC	1102	Db
QY	1162 ACCGATGAGCCG---AGACCTTATTTCAAGGCTCTTCTGACCTGCTAC	1102	Db
Db	1213 ACTGAAGTACTGAAATGACCTGTTGAGATGATCTTCTGACAGGGACATATCAG	1102	Db
QY	1219 TGCCTGGAGAACTGTCGGCTGACTCTCTGAGGAAGGGGGAGACATGTC	1102	Db
Db	1273 TCTCTGGAGAACTGTGTTACTGTGGCTTACCATATTCCGCAAGGGTGGTGTG	1102	Db
QY	1279 ARGACCATGATGGACTCAACAGAGGATGCTCTGCCAATCAGGGCTGACT	1102	Db
Db	1333 AACATGTCGTTGACTGAGACAGAGGGCTGACCAATGCTGGCTGATTT	1102	Db
QY	1339 GAGTCAAGAGGGCAGGGTCTGAGGAGAGGCCAGAGGAGGTCTCGGG	1102	Db
Db	1393 GATTTACTGAGGAAGCTGTCGTTAAGCTGGTGTACCCAGAGGANATCAGAG	1102	Db
QY	1399 GGCATAATGATGACGACATTGAGGGATGACACTCTCTGTAATGCA	1102	Db
Db	1453 GGTATCATGATGATGATCTCTTGTGAGGGATGAAATTCTCTGCTACCA	1102	Db
QY	1459 GTCGGATAGAGGGAGGCCAGGGGGATGCCCTCCAGCAATTCAACAGCT	1102	Db
Db	1513 GTCAAGATGCTGCTGCTGAGCTCAGAGATGCGCATCTGGAGCT	1102	Db
QY	1519 CCCTGCTCTGGCTGCTGCTGAGCTGGCTGGCTGGCTGGCTGGTGTG	1102	Db
Db	1564 GTTCATGACTGCTCTCGATCTCCCTCCACTGCGACTGTAATTTGAT	1102	Db
QY	1579 GACCATGAGGAGCTCTGACTTGTGATGTTACATGTCAGTGTGAGATG	1102	Db
Db	1624 GACCACTGGCATTTACTTTGAGGAACTGTGACTCAGTGTGAGGAGCAT	1102	Db
QY	1639 GTTATGGGGTCAAGGTTCTGGGACATCAGGCCCCGGGTACACTCATGTC	1102	Db

Db 1684 ATCATGGAGGTGAAGTATTGAGACATCTGGAGGAAATGTTATCGTTCCATAT 1743
 Qy 1699 AGGACAGTAGAAGGGACAGCCAAAGGGGGGAGGACTGAGGACTCATGGGAG 1758
 Db 1744 AAACCATCGAAGGAGACTGCCAGAGGGAGATTGGAGACTGTGGAG 1803
 Qy 1759 TCGGAATTCAAGAATGATGAAACTGTGAA 1788
 Db 1804 CTCGAATTCCAGAATGATGAA 1833

RESULT 13
 AA14657 standard: DNA: 1836 BP.
 XX
 AC AA14657;
 XX
 DT 17-OCT-2001 (first entry)
 DE Probe #13343 used to measure gene expression in human placenta sample.
 KW Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder; ss.
 OS Homo sapiens.
 XX
 PN WO20015272-A2.
 XX
 PD 09-AUG-2001.
 XX
 30-JAN-2001; 2001WO-US00663.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207455.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0532366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000US-0024263.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PT Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPT; 2001-488897/53.

PT Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta -
 XX
 PT Claim 25; SEQ ID No 13343; 654pp; English.

CC The present invention relates to single exon nucleic acid probes (SENP).
 CC The present sequence is one such probe. The probes are useful for
 CC producing a microarray for predicting, measuring and displaying gene
 CC expression in samples derived from human placenta. The probes are useful
 CC for antenatal diagnosis of human genetic disorders.

SQ Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other:
 Query Match 28.5%; Score 787.2; DB 22; Length 1836;
 Best Local Similarity 68.3%; Pred. No. 0-216; Mismatches 503; Indels 39; Gaps 4;
 Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4;

Qy 109 GAGGTGCCAACGCAAGGGCAGAACATGAGTCTCTGTCAGGTCATGGACTGCAAGGAG 168
 Db 133 GAGATGGAGGAGGAGGAATGAACTGTGATGACTGGACATATACGTGAA 192
 Qy 169 GCGTCATCTGCACTCTGGPACCCGAGAACCTCTCCCTGGGACAGATGCGCAG 228
 Db 193 GCGGTGATTTCGCCATTGGACCCAAAGACCTCTTGGGACAAATGCTGAGA 252
 Qy 229 GTCATGTCATTGTGGCCCTGATATACATGTCCTGGGGTCCATCATGCTGAC 288

Db 253 GCTACTGTGTTATTGTCGCCATGTTCTGAGCTCTCATGTTCTCATAGCTGAT 312
 Qy 289 CGCTCATGCCATCTATGAGTCATCACTCTCAAGAGGGGGTCRAATAGAA 348
 Db 313 CGGTCATGCTCATAGAACATCACTGAGAACATGTCACATCAAGAAAGAACCTTAAGAA 372
 Qy 349 CCCAATGGAGAACCGACAAACCATTCGGGCTCGGAATGAACTGTCACCTG 408
 Db 373 CCCAATGGAGAACACCAAGAACAGACTGTGAGGATCTGGAAATGAAAGGTTCAACTG 432
 Qy 409 ACCCTTAAGGCCCTGGGTTCTGCTCTGAGATACTCTCTCTTAAATGGGTGTT 468
 Db 433 ACCTTGATGGCCCTGGGACTTCTGTCCTGAGATCTCTTCAGTAATGAGTG 492
 ID AA14657
 XX
 AC AA14657;
 XX
 DT 17-OCT-2001 (first entry)
 DE Probe #13343 used to measure gene expression in human placenta sample.
 KW Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder; ss.
 OS Homo sapiens.
 XX
 PN WO20015272-A2.
 XX
 PD 09-AUG-2001.
 XX
 30-JAN-2001; 2001WO-US00663.
 XX
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-0207455.
 PR 30-JUN-2000; 2000US-0608408.
 PR 03-AUG-2000; 2000US-0532366.
 PR 21-SEP-2000; 2000US-0234687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000US-0024263.
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PT Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPT; 2001-488897/53.

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CC The present invention relates to single exon nucleic acid probes (SENP).
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SQ Sequence 1836 BP; 512 A; 336 C; 464 G; 524 T; 0 other:
 Query Match 28.5%; Score 787.2; DB 22; Length 1836;
 Best Local Similarity 68.3%; Pred. No. 0-216; Mismatches 503; Indels 39; Gaps 4;
 Matches 1168; Conservative 0; Mismatches 503; Indels 39; Gaps 4;

Qy 980 TCCATTCTCTAGTGGAACCTGGTCCCTCTGCCCGGGTCAGATAAGACTGCTC 768
 Db 733 ACHTTCTTCTTCTTCCATCATTTGACTCTGACTCTGTTGCTGTTGGATAGGAGCTCTG 792
 Qy 769 TTCTACAAATACATGCAACAAAGTACCGCACAGACAACACGGAGAAATTCACTAGAG 828
 Db 793 TTATACAGTGTCTACAGAGTATGGGCTGGCACAGAGGGATGATTATGAA 852
 Qy 829 ACAGAGGGTACCCACCC-----TAAAGGCTATGAGATGGATGGAAATGATGAA 879
 Db 853 CATGAGGAGAACGGCATCTCTTAAGACTGAAATGACGAGGGAAACTGGTCAAT 912
 Qy 880 TCCATTCTCTAGTGGAACCTGGTCCCTCTGCCCGGGTCAGATAAGACTGCTC 768
 Db 913 TCTCATGTGAAATATTCTTAGTGGTCTCTGGTCTGGAGGAGGGACCA 972
 Qy 922 GAAGGGGTAGTCCGGAGAGAGATGATCCGGATCTCAAGATCTGAGAACAC 981
 Db 973 GATGATGAGAACGCTAGGGAAATGGCTTAGATGAACTGAGAACATGAGCA 1032
 Qy 982 CCAGAGAAGACTAGTCAGCTGGAGATGCCACTGCTATCATGTCCTTCCACCA 1041
 Db 1033 CCAGATAGAAATAGGCAATTATGAACTTACCTACCAAGGCTTGTGAGCAAC 981
 Qy 1042 CAGAGGAGGCTCTACCGTATCAAGGCACTGCTATGACTGTCAGGCAAT 1101
 Db 1093 CAAAAAAGTAGGCAATTATGCACTGACTGCTCATGACTGGAGCTGGCAAC 1152
 Qy 1102 ATCTGAGAACATCCGAGAACAGCAAGGCCCTCAGCTGAGGGAGTCAC 1161
 Db 1153 ATTTAAAGGGCATGCTGAGCAAGGAGGCTGTCAGCATGCCAGGGCAAC 1212
 Qy 1162 ACCGATGAGCTG---AGGACTTATTCTCAAGGTCCTTGTGACCGATGTTACCA 1218
 Db 1213 ACTGAGGAGCTGAAATGACCTGTTGAGATCTCTTGTGACAGGGACATCA 1272
 Qy 1219 TCTCTGGAGACTGTGGGGCTRACTCTGAGCTGGTGGAGAACGGGGAGACATCA 1278
 Db 1273 TGTCTGGAGACTGTGGTACTGTGGCTTACCATATTCCGAGAGTGAGTTACT 1332
 Qy 1279 AACGACATGATGTGGACTACAAACAGGGATGTTCTGCCAATGGAGGGCTGACTAT 1338

Db	373	CCCATGGAGACCCACCACTGGAGGTGGATGAGCTTACCG
Qy	409	ACCCATATSSCCCTGGTCTCTCTCTCTGAGATCTCCCTCTTATGAGGTGT
Qy	433	ACCTTGATGGCCCTGGATCTCTGCTCTGATGATCTCCCTCTTCTGATGAGGTGT
Db	459	GGTCATGGTCATGCTGGTGTGGATGGACCTTCACATGTTAGGGAGTCAGCT
Qy	493	GGCCATAACTCTACAGCAGGAGCTCGGTCTAGCACACGCGAGTCAGCT
Qy	529	AACATGTTCACTCATGTCATGTCAGTGGACCTTCACATGTTAGGGAGTCAGCT
Qy	553	ATATGTTCACTCATGTCATGTCAGTGGACCTTCACATGTTAGGGAGTCAGCT
Db	585	ATCAGCACTACAGAGTCCTTCATCACCGCTGCTGGAGATATCTTGCCPACATCTGG
Qy	589	ATCAGCACTACAGAGTCCTTCATCACCGCTGCTGGAGATATCTTGCCPACATCTGG
Db	613	ATTAAGCATTTGCGTCTCTTGTGACAGCGCTTGACATCTTGCTACACCTGG
Qy	649	CTCTATGTTCTTCAGTGGCTCCCTGGTGGCTGGAGGTGAGGCTTCCTCC
Db	673	CTTGTACATATTGCTGTCATATCTCTGTCCTGGTGTGTTGAGGCTTCCTCC
Qy	709	ACTCTCTCTCTTCAGTGGCTCCCTGGTGGCTGGAGGTGAGGCTTCCTCC
Qy	733	ACTCTCTCTCTTCACATGTCATGTCATGTCCTGGTGTGCTTGCGTGTGGAGTGGACTCTG
Db	769	TTCTCAATACATGACAAAGTACCGCACAGAACACCGAGGATTATCATGGAG
Qy	793	TTTGTACAGTGTGTACAGAGGTATCGACTGGAGCGACGCTTGCTACACCTGG
Db	829	ACAGAGGGTACCCACCC-----TAAGGCATGAGTGGATGGAAATGATGAT
Qy	853	TCCCAATTCTAGATGGAACCTGTTGCTGGGCCCCCTGGGAAGGGAATGTCAT
Qy	880	TCCCAATTCTAGATGGAACCTGTTGCTGGGCCCCCTGGGAAGGGAATGTCAT
Qy	913	TCTGTGTGAAATTCTAGATGGTCTGGTGTGGAGTGGATGAGGGACCAA
Db	922	GAAGGGTGTAGTCGGCAGAGATGTCGGATCTCAGGATCTGAGCAAACAC
Qy	973	GATGTAGAAGAAGCTGGCGAGAATGCTGGTGTAGGATCTGAGAACCTGAGA
Db	982	CCAGAGGAGCTAGATCACCTGGGAGATGCCATTAGATGCTTCCACCAA
Qy	1033	CCAGATAAGAAATAGAGCAATTAGAAATTAGATGCTTACCTGGAGTCAG
Db	1042	CAGAAGGGCGCGCTCTACCGTATCCAGCCACTCGTGTGAGTGGCAATTAGATGCTTACCTGGAGTCAG
Qy	1093	CAAAAGTAGAGCATTTATGCACTCTGCTCTGAGTCAGCTTACCTGGAGTCAG
Db	1102	ATCCCTGAGAAACATCCAGCAGACAGCCAGAAGGCCCTCCAGCATGAGCGAGTCAG
Qy	1153	ATTTAAGAGGCATGCCGCGTACCAAGGAGCTGTCAGCATGCCGAGTCAG
Db	1162	ACCGAGGAGCTG--AGGACTTATTCAGGCTCTTACCTGGAGTCAG
Qy	1213	ACTGAGTGTACTGAAATGACCCCTGTAGTGTAGATCTCTTACCTGGAGTCAG
Qy	1219	TGCCCTGGAGACTCTGGGCTGTACCTCTGACAGTGGTGGAGAAAGGGAGACATGCA
Db	1273	TGTCTGGAGACTCTGGTGTACTCTGGCCCTTACCATATCCGAGAGGGTGTGAT
Qy	1279	AAGACCATGTTGAGACTACAAACAGAGGATGGTCTGCAATGAGGGCTGACTAT
Db	1393	GAATTACTGAGGACTGTGGTGTAGCCCTGGTGTACCCAGAAATCAGAGTG
Db	1393	AACACTGTGTGACTTCAGAACAGAGGATGGCACAGAACATGCTGGCTGAT
Qy	1399	GGCATATGAGACATTTGAGGAGATGAACTCTTGTAGGTGAGCA
Qy	1339	GAGTCAGGAGACTCTGGTGTACTCTGGCCCTTACCATATCCGAGAGGGTGTG
Qy	1452	1393 GAATTACTGAGGACTGTGGTGTAGCCCTGGTGTACCCAGAAATCAGAGTG
Db	1392	1399 GGCATATGAGACATTTGAGGAGATGAACTCTTGTAGGTGAGCA

CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

Query	Match	21.4%	Score	593.2	DB	23	Length	4546
Best	Local	Similarity	54.7%	Pred.	No.	6.8e-160	Mismatches	1083
Matches	1441	Conservative	0	Mismatches	1083	Indels	108	Gaps
Qy	157	GACTGCAAGGAGGGTCACTCTGCCAATCTGCACTCTGACCGA	--GAACCTTTCCTGCGG	213	Db	623	GAATGTAGCCAGGGCTCTGTCCTGCCACTCTGATGCCAACGCAACATTCGGGGGT	682
Qy	214	GACAAGATGCCAGGGTCACTCTGCTTCTGGCCCTGATAACATGTCCTGGGGT	273	Db	683	GACCGCTCTCCGGCTTGTACTCTGCTCTACTGCCACTCTGATGCCAACGCAACATTCGGGGGT	742	
Qy	274	TCCATCATGCTGACCGCTATGGGACTCTATGAGTCATCACCTCAGAGGGAG	333	Db	743	TCCATCATTCGGAGTCCTCATGGGCCCATCGAGGCAATCACATGATGACGGGG	802	
Qy	334	GTGACAAATTAGAAACCAATGGAGAACAGCACACCAATTGGGGCTGGA	393	Db	803	GTGGGGTCAGGGACCAACACACCAAGCAGGTGATGACGGGGCATCTGGAAAGCA	862	
Qy	394	ACTGCTCCAACTCTGACCCATTGGCCCTGGTCTCTGCTCTGAGACTCTCT	453	Db	863	ACGGTGGCACTAACGCTATGGCCCTGGATCAGTGCCCGCAGATCTGGCT	922	
Qy	454	TTAATGGAGGTGGTCATGGGTCATGCTGGTGTGATCTGGGACCTTACATGTA	513	Db	923	TTAATGGAGGTGGTCATGGGTCATGCTGGTGTGATCTGGGACCTTACATGTA	982	
Qy	514	GGGACTGCAACCTTCACAGATCTCATCATGGCTCTGCTACGTATCCAGAC	573	Db	983	GGATCAGCTCCATCACCTGTTATGATATACGCCATTCAGTGCCCGCAGATCTGGCT	1042	
Qy	574	GGAGAGACTGCAAGATCACCATCACGGCTCTTCATCACCGCTGCTGGAGAT	633	Db	1043	GGCAGGAGTACGGAGGATCCGCATCTGCAGACTCTCTGGTACCCGCTCTCGCT	1102	
Qy	634	TTGGCTACATCTGGCTCTATGATCTGGGAGTCCTCCCTGTGTCCTCCAGTT	693	Db	1103	TTGGCTATCTGGCTCTGCATCTTCATCGTGTTCACCCGGCGTGTCTGGTC	1162	
Qy	694	TGGGAGGCCCTCTCACTCTCTCTTCAGTGTGTCCTCTGGCCGGGGTC	753	Db	1163	TGGGAGGCCATCGTGAATCTCTTCCTCCGCTGACCGTCTGTCGGCCATACATGCC	1222	
Qy	754	GATAAACGACTGCTCTCTCAATACATCACAAAGTACCGCAGAACACCGA	813	Db	1223	GAGCGCGCTCTCTGGCTCAATACATGAGAACACTACCGGGCATAGCGGG	1282	
Qy	814	GGAATTATCATAGAGACAGGGTACCACTAAGGGCATGGATGGATGGAAATG	873	Db	1283	ACCGT-----GGGGCCGGAGACGACGACGACGAGGAG	1330	
Qy	874	ATGAATTCCTCATTTCTAGATGGGAACCTCTGGCCCTGGAGGGAGGTGAG	933	Db	1331	GGCCCAAAACAAACCAATGGTCACATCCGCTCGGGAAACGACGGCCGGCTCGAGGAG	1390	
Qy	934	TCCGGAGAGATGATCCGATTCCTCAGGATCTGAGAACACCCAGAGGGAC	993	Db	1391	GCCCGCTCGCCATGATACACGTTGCTGAGGCTACGCCAGAGTACCCGGCG	1450	
Qy	994	TTAGATCAGCTGGTGGAGATGCCAAATCTATGTCCTTCCACCAACAGAGGAGCGC	1053	Db	1451	CTCGAACAGCTGGAGATGATGCCAGGAGCAGGAGCTGGCTGGCCGGAGCAGTCGGC	1510	
Qy	1054	GCCTCTACCGTATGCCAGGACTCTGATGACGCTGGAGGGCATATCTGA	1108	Db	1511	GCCTCTATGCCATCCAGGCCACCCGCAAGAAGTGGCTGGCGAACCTGATGCGCAAG	1570	

Db	2585	TACGTGAGCCACTCTGTCCTCTTGGAGGTTCTTGTGATTTGGCCCTTCACT	2644
Qy	2230	GAGTACTGGCCACGGCTGGGCTGCTTCGCGCTTCATCCTCATCATGGATGCTAAC	2289
Db	2645	GACATTGCGGCGGCATGTACCTTGTGATTCATGCTCGATGCGCTCATCT	2704
Qy	2290	GCCATCATGGGACCTGGCTCGCAGCTTGGCTGACATCTGGCTCAAGAGTC	2349
Db	2705	GCCATCATGGGAGATGCCGCTCTATTGGCTGCGCTTCAACATCAGGACTGGTA	2764
Qy	2350	ACAGGTGTTTGTGGCATTTGGACCTCTCTCCAGATGTTGCCAACAGCT	2409
Db	2765	ACGGCCATCCCTGTTGTGCGCTTGGCACAAAGCATACATGGCAGCATGATT	2824
Qy	2410	GCTGCCCTCAGGATGTATAGCAGACGCCATGGACAGCTGACGGGAGAACCC	2469
Db	2825	GCGCCAGGATGACGGGGGCCATAATTGGCTCGCATGTACGGCAGCATGG	2884
Qy	2470	GTCAAATGTCCTCCGGCACGGCTGGGCTGGCGTGGCCCATCATCTGGCTTG	2529
Db	2885	GTCAAACGGTGTCTGGCATGGCTGGCTGGACCATGGCCGCTTACACAGCTCC	2944
Qy	2530	CAGGACAGGAGTCACCGTGTCCGGCACACGGCTCTCGTCACCCCTTGACC	2589
Db	2945	CATGGCATGGCTTCAACGGGAGACCGGGAACATTGGATTCGGCTGGCTTGCG	3004
Qy	2590	ATCTTGATTTGTCCTGACAGCTGGCTCTGGTACCGAGGGCGC--CCGACCTGGGA	2646
Db	3005	GGCGAGGCCCTGATGCCATTAATGCTCATTCATGTTCCGGCTGGCACAGGGCATGGC	3064
Qy	2647	GGGGAGCTTGTGGCCCTGGTCAAGCTCCACACATGGCTTGTGAGCTG	2706
Db	3065	GCGAGCTGGCGGTCGAAAGTATGAGTACATCGAGTACATCAGCGAGCATCTGGTATTCCTG	3124
Qy	2707	TGGCTCTCTACACACTTGTGACACTAGAGGGCTATGTACATCAGG	2758
Db	3125	TGGGTTCTCACGGTGTATATGATGATACATGGAGGCTACGAGCTACGGTCATCGGG	3176

Search completed: November 30, 2002, 10:20:30
Job time : 430 secs